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SEQUENCE LISTING

<110> Mueller-Hermelink, Hans Konrad  
Vollmers, Heinz

<120> Neoplasm Specific Antibodies and Uses  
Thereof

<130> 50308/006001

<140> 10/520,224

<141> 2005-01-04

<150> PCT/IB2003/003487

<151> 2003-07-02

<150> DE 10230516.1

<151> 2002-07-06

<150> DE 10229907.2

<151> 2002-07-04

<150> DE 10229906.4

<151> 2002-07-04

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 106

<212> PRT

<213> Homo sapiens

<400> 1

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Thr	Ala	Arg	Ile	Thr	Cys	Ser	Gly	Asp	Ala	Leu	Pro	Lys	Lys	Tyr	Pro
			20					25					30		
Tyr	Trp	Tyr	Gln	Gln	Lys	Ser	Gly	Gln	Ala	Pro	Val	Leu	Val	Ile	Tyr
		35					40						45		
Glu	Asp	Ser	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Ser	Ser	Gly	Thr	Met	Ala	Thr	Leu	Thr	Ile	Ser	Gly	Ala	Gln	Val	Glu
65					70					75				80	
Asp	Glu	Ala	Asp	Tyr	Cys	Tyr	Ser	Thr	Asp	Ser	Ser	Gly	Asn	Met	
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Ser	Ser	Glu	Leu	Gly	Pro	Ser	Ser	Pro	Ser						
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<210> 2

<211> 318

<212> DNA

<213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(318)

<400> 2  
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 Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln  
 1 5 10 15  
 acg gcc agg atc acc tgc tct gga gat gca ttg cca aaa aaa tat cct 96  
 Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Lys Lys Tyr Pro  
 20 25 30  
 tat tgg tac cag cag aag tca ggc cag gcc cct gtg ctg gtc atc tat 144  
 Tyr Trp Tyr Gln Gln Lys Ser Gly Gln Ala Pro Val Leu Val Ile Tyr  
 35 40 45  
 gag gac agc aaa cga ccc tcc ggg atc cct gag aga ttc tct ggc tcc 192  
 Glu Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser  
 50 55 60  
 agc tca ggg aca atg gcc acc ttg act atc agt ggg gcc cag gtg gag 240  
 Ser Ser Gly Thr Met Ala Thr Leu Thr Ile Ser Gly Ala Gln Val Glu  
 65 70 75 80  
 gat gaa gct gac tac tac tgt tac tca aca gac agc agt ggt aat atg 288  
 Asp Glu Ala Asp Tyr Cys Tyr Ser Thr Asp Ser Ser Gly Asn Met  
 85 90 95  
 tct tcg gaa ctg gga cca agc tca ccg tcc 318  
 Ser Ser Glu Leu Gly Pro Ser Ser Pro Ser  
 100 105

<210> 3  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 3  
 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser  
 1 5 10 15  
 Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp  
 20 25 30  
 Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser  
 35 40 45  
 Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu  
 50 55 60  
 Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr  
 65 70 75 80  
 Cys Ala Lys Asp Ser Phe Arg Glu Gly Pro Trp Gly Gln Gly Thr Leu  
 85 90 95  
 Val Thr

<210> 4  
 <211> 294  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(294)

<400> 4  
 ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agc agc 48  
 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser  
 1 5 10 15  
 tat gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg 96  
 Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp  
 20 25 30  
 gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca gac tcc 144  
 Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser  
 35 40 45  
 gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg ctg 192  
 Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu  
 50 55 60  
 tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta tat tac 240  
 Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr  
 65 70 75 80  
 tgt gcg aaa gat tca ttt cgt gaa gga ccc tgg ggc cag gga acc ctg 288  
 Cys Ala Lys Asp Ser Phe Arg Glu Gly Pro Trp Gly Gln Gly Thr Leu  
 85 90 95  
 gtc acc 294  
 Val Thr

<210> 5  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 5  
 Gln Ser Ala Leu Thr Gln Pro Ala Ser Leu Ser Ala Ser Pro Gly Ala  
 1 5 10 15  
 Ser Ala Ser Leu Thr Cys Thr Leu Arg Ser Gly Ile Asn Val Gly Thr  
 20 25 30  
 Tyr Arg Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln Tyr  
 35 40 45  
 Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Lys Gly Ser Gly Val  
 50 55 60  
 Pro Ser Arg Phe Ser Gly Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile  
 65 70 75 80  
 Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys  
 85 90 95

Met Ile Trp His Ser Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu  
                   100                  105                  110  
 Thr Val Leu Gly  
                   115

<210> 6  
 <211> 348  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(348)

<400> 6  
 cag tct gcc ctg act cag cct gct tcc ctc tct gca tct cct gga gca 48  
 Gln Ser Ala Leu Thr Gln Pro Ala Ser Leu Ser Ala Ser Pro Gly Ala  
   1                  5                  10                  15  
  
 tca gcc agt ctc acc tgc acc ttg cgc agt ggc atc aat gtt ggt acc 96  
 Ser Ala Ser Leu Thr Cys Thr Leu Arg Ser Gly Ile Asn Val Gly Thr  
                   20                  25                  30  
  
 tac agg ata tac tgg tac cag cag aag cca ggg agt cct ccc cag tat 144  
 Tyr Arg Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln Tyr  
                   35                  40                  45  
  
 ctc ctg agg tac aaa tca gac tca gat aag cag aag ggc tct gga gtc 192  
 Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Lys Gly Ser Gly Val  
   50                  55                  60  
  
 ccc agc cgc ttc tct gga tcc aaa gat gct tcg gcc aat gca ggg att 240  
 Pro Ser Arg Phe Ser Gly Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile  
   65                  70                  75                  80  
  
 tta ctc atc tct ggg ctc cag tct gag gat gag gct gac tat tac tgt 288  
 Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys  
                   85                  90                  95  
  
 atg att tgg cac agc agc gct tgg gtg ttc ggc gga ggg acc aag ctg 336  
 Met Ile Trp His Ser Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu  
                   100                  105                  110  
  
 acc gtc cta ggt 348  
 Thr Val Leu Gly  
                   115

<210> 7  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 7  
 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser  
   1                  5                  10                  15

Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp  
                   20                  25                  30  
 Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser  
                   35                  40                  45  
 Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu  
                   50                  55                  60  
 Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr  
                   65                  70                  75                  80  
 Cys Ala Lys Gly Gly Ala Glu Gly Trp Tyr Glu Tyr Tyr Tyr Tyr Tyr  
                   85                  90                  95  
 Gly Met Asp Val Trp Gly Gln Gly Thr Leu Val  
                   100                  105

<210> 8  
 <211> 321  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(321)

<400> 8  
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 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser  
   1                  5                  10                  15  
  
 tat gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg 96  
 Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp  
                   20                  25                  30  
  
 gtc tca gct att agt ggt agt ggt ggt agt aca tac tac gca gac tcc 144  
 Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser  
                   35                  40                  45  
  
 gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg ctg 192  
 Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu  
                   50                  55                  60  
  
 tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta tat tac 240  
 Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr  
                   65                  70                  75                  80  
  
 tgt gcg aaa ggt ggg gcc gaa ggc tgg tac gag tac tac tac tac tac 288  
 Cys Ala Lys Gly Gly Ala Glu Gly Trp Tyr Glu Tyr Tyr Tyr Tyr Tyr  
                   85                  90                  95  
  
 ggt atg gac gtc tgg ggc caa ggg acc ctg gtc 321  
 Gly Met Asp Val Trp Gly Gln Gly Thr Leu Val  
                   100                  105

<210> 9  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 9  
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Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr  
20 25 30  
Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu  
35 40 45  
Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe  
50 55 60  
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu  
65 70 75 80  
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Lys Arg Ser Ser  
85 90 95  
Asn Thr Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu  
100 105 110

<210> 10  
<211> 330  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(330)

<400> 10  
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Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln  
1 5 10 15  
tcg atc acc atc tcc tgc act gga acc agc agt gac gtt ggt ggt tat 96  
Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr  
20 25 30  
aac tat gtc tcc tgg tac caa cag cac cca ggc aaa gcc ccc aaa ctc 144  
Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu  
35 40 45  
atg att tat gat gtc agt aat cgg ccc tca ggg gtt tct aat cgc ttc 192  
Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe  
50 55 60  
tct ggc tcc aag tct ggc aac acg gcc tcc ctg acc atc tct gga ctc 240  
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu  
65 70 75 80  
cag gct gag gac gag gct gat tac tac tgc agc tca aaa aga agc agc 288  
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Lys Arg Ser Ser  
85 90 95  
aac act cta gta ttc ggc gga ggg acc aag ctg acc gtc cta 330  
Asn Thr Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu  
100 105 110

<210> 11  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 11  
 Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr  
 1 5 10 15  
 Ser Phe Thr Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys  
 20 25 30  
 Gly Leu Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg  
 35 40 45  
 Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Thr Ser  
 50 55 60  
 Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr  
 65 70 75 80  
 Ala Ile Tyr Tyr Cys Ala Arg Glu Val Tyr Thr Gly Arg Asn Tyr Tyr  
 85 90 95  
 Tyr Tyr Gly Leu Asp Val Trp Gly Gln Gly Thr Leu Val  
 100 105

<210> 12  
 <211> 327  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(327)

<400> 12  
 aaa aag ccc ggg gag tct ctg agg atc tcc tgt aag ggc tct gga tac 48  
 Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr  
 1 5 10 15  
 agt ttt acc acc tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa 96  
 Ser Phe Thr Thr Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys  
 20 25 30  
 ggc ctg gag tgg atg ggg atc atc tat cct ggt gac tct gat acc aga 144  
 Gly Leu Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg  
 35 40 45  
 tac agc ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac acg tcc 192  
 Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Thr Ser  
 50 55 60  
 atc agt acc gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc 240  
 Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr  
 65 70 75 80  
 gcc ata tat tac tgt gcg agg gag gtc tat act ggc cga aac tac tac 288  
 Ala Ile Tyr Tyr Cys Ala Arg Glu Val Tyr Thr Gly Arg Asn Tyr Tyr  
 85 90 95

tac tac ggt ctg gac gtc tgg ggc caa gga acc ctg gtc  
Tyr Tyr Gly Leu Asp Val Trp Gly Gln Gly Thr Leu Val  
100 105

327

8